In the Specification:

Please amend the specification at page 4, lines 6-10 as follows:

Fig. 1 is the nucleotide sequence and the deduced amino acid sequence of a bovine tumor necrosis factor receptor-I (TNF-RI) cDNA (SEQ ID NO:1; GenBank Accession No. U90937). A solid line indicates the hydrophobic signal peptide and a dashed line indicates the transmembrane region. Within the extracellular domain, the cysteine residues are circled and N-linked glycosylation sites are boxed.

Please amend the specification at page 6, lines 3-16 as follows:

Generally, percent sequence identity is calculated by determining the number of matched positions in aligned nucleic acid sequences, dividing the number of matched positions by the total number of aligned nucleotides, and multiplying by 100. A matched position refers to a position in which identical nucleotides occur at the same position in aligned nucleic acid sequences. Nucleic acid sequences can be aligned by visual inspection, or by using sequence alignment software, such as the Sequence Analysis Software Package of the Genetics Computer Group, University of Wisconsin Biotechnology Center, 1710 University Avenue, Madison, WI 53705, or BLAST programs (provided as a service by the National Center for Biotechnology Information, on the world wide web at ncbi.nlm.nih.gov ~~www.ncbi.nlm.nih.gov~~). The programs are described in detail by Karlin et al., *Proc Natl Acad Sci USA* 87:2264 (1990) and 90:5873 (1993), and Altschul et al., *Nucl Acids Res* 25:3389 (1997). Typically, default parameters and algorithms are used when performing sequence analysis. Sequence analysis of TNF-RI as described herein was performed using BestFit (with a Gap Weight of 5.0 and 3.0 and a Length Weight of 0.3 and 0.1 for nucleic acids and amino acids, respectively).

Please amend the specification at page 16, lines 16-29 as follows:

TNF inhibition assays were performed as described in the CellTiter 96™ Non-Radioactive Cell Proliferation Assay (Promega, Madison, WI) ~~(www.Promega.com/tbs/tb112/tb112.html)~~ with slight modifications. Briefly, two-fold serial dilutions of soluble bovine TNF-RI or anti-bovine TNF-α monoclonal antibody (MAb) BC9 (courtesy of Dr. Jan Naessens, International Livestock Research Institute, Nairobi, Kenya) were

incubated for 1 h at room temperature with equal volumes of bovine whey samples (Shuster et al., 1993, *Am. J. Vet. Res.* 54:80-85) from milk obtained from quarters that had been infused with lipopolysaccharide (LPS) from *Escherichia coli* serotype 055:B5 (Sigma, St. Louis, Mo, USA). The samples were then assayed in triplicate for cytotoxicity on WEHI 164 mouse fibrosarcoma cells (clone 13), seeded at a concentration of 3×10^4 cells/well in RPMI-1640 medium (Sigma) supplemented with 10% heat-inactivated fetal bovine serum (Hyclone Laboratories, Logan, UT) and 50 μg gentamicin/ml (Sigma). A recombinant murine TNF-α was used as a standard to calculate TNF-α cytotoxicity in the samples. Absorbances were read at a wavelength of 590 nm and corrected for background absorbances using a reference wavelength of 650 nm.